

WHAT IS CLAIMED IS:

1. An isolated polypeptide comprising a sequence of amino acid residues that is at least 80% identical in amino acid sequence to residues 31-346 of SEQ ID NO:2, wherein said sequence comprises cysteine residues corresponding to residues 58, 65, 132, 147, 153 and 219 of SEQ ID NO:2.

2. An isolated polypeptide according to claim 1, wherein said polypeptide is at least 90% identical in amino acid sequence to residues 29-346 of SEQ ID NO:2, wherein said sequence comprises cysteine residues corresponding to residues 58, 65, 132, 147, 153 and 219 of SEQ ID NO:2.

3. An isolated polypeptide according to claim 2, wherein said polypeptide comprises residues 1-346 of SEQ ID NO:2.

4. An isolated polypeptide according to claim 1, covalently linked amino terminally or carboxy terminally to a moiety selected from the group consisting of: affinity tags, toxins, radionucleotides, enzymes and fluorophores.

5. An isolated polypeptide having a sequence of amino acid residues selected from the group consisting of:

- a) a sequence of amino acid residues from amino acid residue 1 to amino acid residue 37 of SEQ ID NO: 2;
- b) a sequence of amino acid residues from amino acid residue 29 to amino acid residue 37 of SEQ ID NO: 2;
- c) a sequence of amino acid residues from amino acid residue 31 to amino acid residue 37 of SEQ ID NO: 2;
- d) a sequence of amino acid residues from amino acid residue 29 to amino acid residue 45 of SEQ ID NO: 2;
- e) a sequence of amino acid residues from amino acid residue 31 to amino acid residue 45 of SEQ ID NO: 2;

- f) a sequence of amino acid residues from amino acid residue 40 to amino acid residue 45 of SEQ ID NO: 2;
- g) a sequence of amino acid residues from amino acid residue 40 to amino acid residue 346 of SEQ ID NO: 2;
- h) a sequence of amino acid residues from amino acid residue 48 to amino acid residue 346 of SEQ ID NO: 2;
- i) a sequence of amino acid residues from amino acid residues 29 to amino acid residue 276 of SEQ ID NO:2;
- j) a sequence of amino acid residues from amino acid residues 31 to amino acid residue 276 of SEQ ID NO:2;
- k) a sequence of amino acid residues from amino acid residues 40 to amino acid residue 276 of SEQ ID NO:2;
- l) a sequence of amino acid residues from amino acid residues 48 to amino acid residue 276 of SEQ ID NO:2;
- m) a sequence of amino acid residues from amino acid residue 278 to amino acid residue 346 of SEQ ID NO: 2; and
- n) a sequence of amino acid residues that is at least 80% identical in amino acid sequence to a), b), c), d), e), f), g), h), i), j), k), l) or m).

6. A fusion protein consisting essentially of a first portion and a second portion joined by a peptide bond, said first portion comprising a polypeptide that is at least 80% identical in amino acid sequence to the amino acid sequence of a polypeptide selected from the group consisting of:

- a) a sequence of amino acid residues from amino acid residue 1 to amino acid residue 37 of SEQ ID NO: 2;
- b) a sequence of amino acid residues from amino acid residue 29 to amino acid residue 37 of SEQ ID NO: 2;
- c) a sequence of amino acid residues from amino acid residue 31 to amino acid residue 37 of SEQ ID NO: 2;
- d) a sequence of amino acid residues from amino acid residue 29 to amino acid residue 45 of SEQ ID NO: 2;
- e) a sequence of amino acid residues from amino acid residue 31 to amino acid residue 45 of SEQ ID NO: 2;

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f) a sequence of amino acid residues from amino acid residue 40 to amino acid residue 45 of SEQ ID NO: 2;

g) a sequence of amino acid residues from amino acid residue 40 to amino acid residue 346 of SEQ ID NO: 2;

h) a sequence of amino acid residues from amino acid residue 48 to amino acid residue 346 of SEQ ID NO: 2;

i) a sequence of amino acid residues from amino acid residues 29 to amino acid residue 276 of SEQ ID NO:2;

j) a sequence of amino acid residues from amino acid residues 31 to amino acid residue 276 of SEQ ID NO:2;

k) a sequence of amino acid residues from amino acid residues 40 to amino acid residue 276 of SEQ ID NO:2;

l) a sequence of amino acid residues from amino acid residues 48 to amino acid residue 276 of SEQ ID NO:2;

m) a sequence of amino acid residues from amino acid residue 278 to amino acid residue 346 of SEQ ID NO: 2;

o) a sequence of amino acid residues from amino acid residue 1 to amino acid residue 346 of SEQ ID NO: 2;

p) a sequence of amino acid residues from amino acid residue 29 to amino acid residue 346 of SEQ ID NO: 2; and

q) a sequence of amino acid residues from amino acid residue 31 to amino acid residue 346 of SEQ ID NO: 2; and said second portion comprising another polypeptide.

7. A fusion protein comprising a secretory signal sequence having the amino acid sequence of amino acid residues 1-28 or 1-30 of SEQ ID NO:2, wherein said secretory signal sequence is operably linked to an additional polypeptide.

8. An isolated protein comprising a first polypeptide that is at least 80% identical in amino acid sequence to the amino acid sequence of a polypeptide selected from the group consisting of:

a) amino acid residues 1-29 of SEQ ID NO:2, said polypeptide comprising a cysteine residue at a position corresponding to residue 15 of SEQ ID NO:2;

b) amino acid residues 1-30 of SEQ ID NO:2, said polypeptide comprising a cysteine residue at a position corresponding to residue 15 of SEQ ID NO:2;

c) amino acid residues 48-276 of SEQ ID NO:2, said polypeptide comprising cysteine residues at positions corresponding to residues 58, 65, 132, 147, 153 and 219 of SEQ ID NO:2; and

d) amino acid residues 31-346 of SEQ ID NO:2, said polypeptide comprising cysteine residues at positions corresponding to residues 58, 65, 132, 147, 153 and 219 of SEQ ID NO:2;

complexed to a second polypeptide.

9. An isolated protein according to claim 8, wherein said first polypeptides and said second polypeptide are complexed by intermolecular disulfide bonds.

10. An isolated protein according to claim 9, wherein said protein is a homodimer.

11. An isolated protein according to claim 9, wherein said protein is a heterodimer.

12. An expression vector comprising the following operably linked elements:

a transcription promoter;

a DNA segment encoding a polypeptide comprising a sequence of amino acid residues that is at least 80% identical in amino acid sequence to residues 31-346 of SEQ ID NO:2, wherein said sequence comprises cysteine residues corresponding to residues 58, 65, 132, 147, 153 and 219 of SEQ ID NO:2; and

a transcription terminator.

13. An expression vector according to claim 12, wherein said DNA segment encodes a polypeptide that is at

least 90% identical in amino acid sequence to residues 29-346 of SEQ ID NO:2 wherein said sequence comprises cysteine residues corresponding to residues 58, 65, 132, 147, 153 and 219 of SEQ ID NO:2.

14. An expression vector according to claim 13, wherein said DNA segment encodes a polypeptide comprising residues 1-346 of SEQ ID NO:2.

15. An expression vector according to claim 12, wherein said DNA segment encodes a polypeptide covalently linked amino terminally or carboxy terminally to an affinity tag.

16. An expression vector according to claim 12 wherein said DNA segment further encodes a secretory signal sequence operably linked to said polypeptide.

17. An expression vector according the claim 16, wherein said secretory signal sequence comprises residues 1-28 or 1-30 of SEQ ID NO:2.

18. A cultured cell into which has been introduced an expression vector comprising the following operably linked elements:

a transcription promoter;

a DNA segment encoding a polypeptide comprising a sequence of amino acid residues that is at least 80% identical in amino acid sequence to residues 31-346 of SEQ ID NO:2, wherein said sequence comprises cysteine residues corresponding to residues 58, 65, 132, 147, 153 and 219 of SEQ ID NO:2; and

a transcription terminator, wherein said cell expresses said polypeptide encoded by said DNA segment.

19. A method of producing a polypeptide comprising:
culturing a cell into which has been introduced an
expression vector comprising the following operably linked
elements:

a transcription promoter;

a DNA segment encoding a polypeptide comprising a
sequence of amino acid residues that is at least 80% identical
in amino acid sequence to residues 31-346 of SEQ ID NO:2,
wherein said sequence comprises cysteine residues
corresponding to residues 58, 65, 132, 147, 153 and 219 of SEQ
ID NO:2; and

a transcription terminator;

whereby said cell expresses said polypeptide encoded
by said DNA segment; and
recovering said expressed polypeptide.

20. A pharmaceutical composition comprising a
polypeptide, said polypeptide comprising a sequence of amino
acid residues that is at least 80% identical in amino acid
sequence to residues 31-346 of SEQ ID NO:2, wherein said
sequence comprises cysteine residues corresponding to residues
58, 65, 132, 147, 153 and 219 of SEQ ID NO:2;

in combination with a pharmaceutically acceptable
vehicle.

21. An antibody that specifically binds to an
epitope of a polypeptide comprising a sequence of amino acid
residues that is at least 80% identical in amino acid sequence
to residues 31-346 of SEQ ID NO:2, wherein said sequence
comprises cysteine residues corresponding to residues 58, 65,
132, 147, 153 and 219 of SEQ ID NO:2.

22. A binding protein that specifically binds to
an epitope of a polypeptide comprising a sequence of amino
acid residues that is at least 80% identical in amino acid
sequence to residues 31-346 of SEQ ID NO:2, wherein said

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23. An isolated polynucleotide encoding a polypeptide comprising a sequence of amino acid residues that is at least 80% identical in amino acid sequence to residues 31-346 of SEQ ID NO:2, wherein said sequence comprises cysteine residues corresponding to residues 58, 65, 132, 147, 153 and 219 of SEQ ID NO:2.

25. An isolated polynucleotide according to claim 24, wherein said polypeptide comprises residues 1-346 of SEQ ID NO:2.

27. An isolated polynucleotide selected from the group consisting of:

b) a sequence of nucleotides from nucleotide 131 to nucleotide 157 of SEQ ID NO:1;

d) a sequence of nucleotides from nucleotide 131 to nucleotide 181 of SEQ ID NO:1;

e) a sequence of nucleotides from nucleotide 137 to nucleotide 181 of SEQ ID NO:1;

j) degenerate nucleotide sequences of a), b), c), d), e), f), g), h) or i).

g) degenerate nucleotide sequences of a), b), c), d), e) or f).

a) a sequence of amino acid residues from amino acid residue 1 to amino acid residue 37 of SEQ ID NO: 2;

said second portion comprising another polypeptide.

30. An isolated polynucleotide encoding a fusion protein comprising a secretory signal sequence having the amino acid sequence of amino acid residues 1-28 or 1-30 of SEQ

31. An isolated polynucleotide comprising the sequence of nucleotide 1 to nucleotide 1084 of SEQ ID NO:13.

33. A method for detecting a genetic abnormality in a patient, comprising:

obtaining a genetic sample from a patient;
incubating the genetic sample with a polynucleotide comprising at least 14 contiguous nucleotides of SEQ ID NO:1 or the complement of SEQ ID NO:1, under conditions wherein said polynucleotide will hybridize to complementary polynucleotide sequence, to produce a first reaction product;
comparing said first reaction product to a control reaction product, wherein a difference between said first reaction product and said control reaction product is indicative of a genetic abnormality in the patient.